CLAIM AMENDMENTS

1. (currently amended) A method of ~~identifying~~ obtaining and organizing information about a plurality of unknown raw nucleic acid ~~sequence~~ sequences, comprising:

a) creating a directory of files in a computer, for storing information related to the plurality of unknown raw nucleic acid ~~sequence~~ sequences;

b) inputting ~~a~~ the plurality of unknown raw nucleic acid ~~sequence~~ sequences into the computer;

c) automatically determining trimming locations of each unknown raw nucleic acid sequence using a best match type scoring algorithm which, during each scoring operation, allows for nucleotide mismatches and allows either a single nucleotide insertion or a single nucleotide deletion in the unknown raw nucleic acid sequence, the scoring algorithm first comparing a known positive 5' adapter sequence and a known negative 5' adapter sequence to the raw nucleic acid sequence and assigning a 5' trimming location to a position in the unknown raw nucleic acid sequence having the highest score and determining an insertion orientation according to the higher scoring of the known positive and negative 5' adapter sequences, then comparing a known 3' adapter sequence having a same orientation as the higher scoring known 5' adapter sequence to the unknown raw nucleic acid sequence and assigning a 3' trimming location to a position in the unknown raw nucleic acid sequence having the highest score, then comparing a known positive confirmation sequence and a known negative confirmation sequence to the raw nucleic acid sequence and assigning a confirmation sequence location to a position in the unknown raw nucleic acid sequence having the highest score and determining a sequencing direction according to the higher scoring of the known positive and negative confirmation sequences, and then trimming each of the plurality of unknown raw nucleic acid ~~sequence~~ sequences to obtain a respective plurality of trimmed unknown nucleic acid ~~sequence~~ sequences;

d) submitting each of the plurality of trimmed unknown nucleic acid ~~sequence~~ sequences electronically to a nucleic acid identification database having a search program, the search program producing search results based on similarity of a trimmed unknown nucleic acid sequence to a known nucleic acid sequence, and receiving the search results for each of the plurality of trimmed unknown nucleic acid sequences electronically from the nucleic acid identification database;

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e) <u>automatically</u> choosing selective information, <u>including similar known nucleic acid</u> <u>sequences,</u> from each search result and <u>automatically</u> inserting the selective information from each search result into a <u>respective</u> first electronic spreadsheet;

f) selecting at least one of the search results from <u>each of</u> the <u>respective</u> first electronic ~~spreadsheet~~ <u>spreadsheets</u> and <u>automatically</u> inserting the <u>selective information about the</u> at least one search result into a second electronic spreadsheet.

2. (original) The method of claim 1 wherein said nucleic acid identification database is publicly accessible via the Internet.

3. (currently amended) The method of claim 2 wherein said nucleic acid identification database ~~is~~ <u>comprises</u> the National Center for Biotechnological Information ~~database~~ <u>databases</u>.

4. (currently amended) The method of claim 1 wherein the <u>plurality of unknown</u> raw nucleic acid ~~sequence~~ <u>sequences</u> in step b) ~~is~~ <u>are</u> in electronic form.

5. (currently amended) The method of claim 1 wherein step a) includes creating seven main directories comprising a raw nucleic acid sequence directory for storing <u>the plurality of unknown</u> raw nucleic acid sequences from step b), a trimmed nucleic acid sequence directory for storing <u>the plurality of</u> trimmed <u>unknown</u> nucleic acid sequences from step c), a trimming parameters directory for storing trimming parameters used in step c), a nucleic acid identification database search results directory for storing the search results from step d), a first electronic spreadsheet directory for storing ~~the selective information from~~ <u>first electronic spreadsheets generated in</u> step e), a second electronic spreadsheet directory for storing the ~~at least one search result from~~ <u>second electronic spreadsheet generated in</u> step f), a vector directory for storing vector definitions and a temporary file storage directory for temporarily storing files.

6. (original) The method of claim 5 further comprising creating a DNA library subdirectory in each of the raw nucleic acid sequence directory, the trimmed nucleic acid sequence directory, the trimming parameters directory and the nucleic acid identification database search results directory.

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7. (currently amended) The method of claim 1 wherein step d) is performed at a preset later time and then steps e) and f) are performed.

8. (canceled)

9. (currently amended) The method of claim 1 wherein the second electronic spreadsheet in step f) includes hyperlinks to the first electronic spreadsheet spreadsheets in step e), the search results in step d) and the nucleic acid identification database in step d).

10. (original) The method of claim 1 wherein the search results in step d) are received in the form of an html file.

11. (currently amended) The method of claim 10 wherein the selective information in step e) includes a particular database that was searched, a hyperlink to the html file, a hyperlink to the nucleic acid identification database, a score that represents the number of nucleotides matching between the trimmed unknown nucleic acid sequence and a the known nucleic acid sequence stored in the nucleic acid identification database, an E value that represents the probability that a random sequence of nucleotides having a length equal to a length of the trimmed unknown nucleic acid sequence would match the known nucleic acid sequence stored in the nucleic acid identification database and a textual description of the known nucleic acid sequence stored in the nucleic acid identification database.

12. (canceled)

13. (currently amended) The method of claim 12 1 wherein the trimming positions locations are adjustable by a user using a Trimming Interface display.

14. (currently amended) The method of claim 1 wherein step d) includes submitting the plurality of trimmed unknown nucleic acid sequence sequences and receiving the search results using a web browser program and the Internet.

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15. (currently amended) The method of claim 13 wherein the Trimming Interface display includes scroll bars for adjusting the trimming ~~positions~~ locations.

16. (canceled)

17. (canceled)

18. (original) The method of claim 1 wherein in step f) the computer automatically selects the at least one search result and inserts it into the second electronic spreadsheet.

19. (original) The method of claim 1 wherein in step f) a user selects the at least one search result.

20. (original) A computer readable medium containing a computer program for performing the method of claim 1.

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